OIPE

#2

RAW SEQUENCE LISTING DATE: 10/10/2001
PATENT APPLICATION: US/09/960,643 TIME: 12:54:43

Input Set : A:\Seqlist.txt
Output Set: N:\CRF3\10102001\I960643.raw

ENTERED

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      4 <110> APPLICANT: Yoganathan, Thillainathan
      5       Delaney, Allen
      7 <120> TITLE OF INVENTION: CAMK-X1 and its Uses
     10 <130> FILE REFERENCE: KINE024
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/960,643
C--> 13 <141> CURRENT FILING DATE: 2001-09-21
     15 <160> NUMBER OF SEQ ID NOS: 13
     17 <170> SOFTWARE: FastSEQ for Windows Version 4.0
     19 <210> SEQ ID NO: 1
     20 <211> LENGTH: 2447
     21 <212> TYPE: DNA
     22 <213> ORGANISM: H. sapiens
     24 <220> FEATURE:
     25 <221> NAME/KEY: CDS
     26 <222> LOCATION: (70)...(1498)
     28 <400> SEQUENCE: 1
     29 tggagtggga gctcaagcag gattcttccc gagtccctgg catcctcaga agcttcaact     60
     30 ctggaggca atg ggt cga aag gaa gaa gat gac tgc agt tcc tgg aag aaa    111
     31           Met Gly Arg Lys Glu Glu Asp Asp Cys Ser Ser Trp Lys Lys
     32            1               5                  10
     34 cag acc acc aac atc cgg aaa acc ttc att ttt atg gaa gtg ctg gga     159
     35 Gln Thr Thr Asn Ile Arg Lys Thr Phe Ile Phe Met Glu Val Leu Gly
     36  15                  20                  25                  30
     38 tca gga gct ttc tca gaa gtt ttc ctg gtg aag caa aga ctg act ggg     207
     39 Ser Gly Ala Phe Ser Glu Val Phe Leu Val Lys Gln Arg Leu Thr Gly
     40                  35                  40                  45
     42 aag ctc ttt gct ctg aag tgc atc aag aag tca cct gcc ttc cgg gac     255
     43 Lys Leu Phe Ala Leu Lys Cys Ile Lys Lys Ser Pro Ala Phe Arg Asp
     44              50                  55                  60
     46 agc agc ctg gag aat gag att gct gtg ttg aaa aag atc aag cat gaa     303
     47 Ser Ser Leu Glu Asn Glu Ile Ala Val Leu Lys Lys Ile Lys His Glu
     48          65                  70                  75
     50 aac att gtg acc ctg gag gac atc tat gag agc acc acc cac tac tac     351
     51 Asn Ile Val Thr Leu Glu Asp Ile Tyr Glu Ser Thr Thr His Tyr Tyr
     52      80                  85                  90
     54 ctg gtc atg cag ctt gtt tct ggt ggg gag ctc ttt gac cgg atc ctg     399
     55 Leu Val Met Gln Leu Val Ser Gly Gly Glu Leu Phe Asp Arg Ile Leu
     56  95                  100                 105                 110
     58 gag cgg ggt gtc tac aca gag aag gat gcc agt ctg gtg atc cag cag     447
     59 Glu Arg Gly Val Tyr Thr Glu Lys Asp Ala Ser Leu Val Ile Gln Gln
     60                  115                 120                 125
     62 gtc ttg tcg gca gtg aaa tac cta cat gag aat ggc atc gtc cac aga     495
     63 Val Leu Ser Ala Val Lys Tyr Leu His Glu Asn Gly Ile Val His Arg
     64              130                 135                 140
     66 gac tta aag ccc gaa aac ctg ctt tac ctt acc cct gaa gag aac tct     543
     67 Asp Leu Lys Pro Glu Asn Leu Leu Tyr Leu Thr Pro Glu Glu Asn Ser
     68          145                 150                 155
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70 aag atc atg atc act gac ttt ggt ctg tcc aag atg gaa cag aat ggc      591
71 Lys Ile Met Ile Thr Asp Phe Gly Leu Ser Lys Met Glu Gln Asn Gly
72     160                 165                 170
74 atc atg tcc act gcc tgt ggg acc cca ggc tac gtg gct cca gaa gtg      639
75 Ile Met Ser Thr Ala Cys Gly Thr Pro Gly Tyr Val Ala Pro Glu Val
76 175                 180                 185                 190
78 ctg gcc cag aaa ccc tac agc aag gct gtg gat tgc tgg tcc atc ggc      687
79 Leu Ala Gln Lys Pro Tyr Ser Lys Ala Val Asp Cys Trp Ser Ile Gly
80                 195                 200                 205
82 gtc atc acc tac ata ttg ctc tgt gga tac ccc ccg ttc tat gaa gaa      735
83 Val Ile Thr Tyr Ile Leu Leu Cys Gly Tyr Pro Pro Phe Tyr Glu Glu
84             210                 215                 220
86 acg gag tct aag ctt ttc gag aag atc aag gag ggc tac tat gag ttt      783
87 Thr Glu Ser Lys Leu Phe Glu Lys Ile Lys Glu Gly Tyr Tyr Glu Phe
88         225                 230                 235
90 gag tct cca ttc tgg gat gac att tct gag tca gcc aag gac ttt att      831
91 Glu Ser Pro Phe Trp Asp Asp Ile Ser Glu Ser Ala Lys Asp Phe Ile
92     240                 245                 250
94 tgc cac ttg ctt gag aag gat ccg aac gag cgg tac acc tgt gag aag      879
95 Cys His Leu Leu Glu Lys Asp Pro Asn Glu Arg Tyr Thr Cys Glu Lys
96 255                 260                 265                 270
98 gcc ttg agt cat ccc tgg att gac gga aac acg gcc ctc cac cgg gac      927
99 Ala Leu Ser His Pro Trp Ile Asp Gly Asn Thr Ala Leu His Arg Asp
100                275                 280                 285
102 atc tac cca tca gtc agc ctc cag atc cag aag aac ttt gct aag agc      975
103 Ile Tyr Pro Ser Val Ser Leu Gln Ile Gln Lys Asn Phe Ala Lys Ser
104             290                 295                 300
106 aag tgg agg caa gcc ttc aac gca gca gct gtg gtg cac cac atg agg     1023
107 Lys Trp Arg Gln Ala Phe Asn Ala Ala Ala Val Val His His Met Arg
108         305                 310                 315
110 aag cta cac atg aac ctg cac agc ccg ggc gtc cgc cca gag gtg gag     1071
111 Lys Leu His Met Asn Leu His Ser Pro Gly Val Arg Pro Glu Val Glu
112     320                 325                 330
114 aac agg ccg cct gaa act caa gcc tca gaa acc tct aga ccc agc tcc     1119
115 Asn Arg Pro Pro Glu Thr Gln Ala Ser Glu Thr Ser Arg Pro Ser Ser
116 335                 340                 345                 350
118 cct gag atc acc atc acc gag gca cct gtc ctg gac cac agt gta gca     1167
119 Pro Glu Ile Thr Ile Thr Glu Ala Pro Val Leu Asp His Ser Val Ala
120                355                 360                 365
122 ctc cct gcc ctg acc caa tta ccc tgc cag cat ggc cgc cgg ccc act     1215
123 Leu Pro Ala Leu Thr Gln Leu Pro Cys Gln His Gly Arg Arg Pro Thr
124             370                 375                 380
126 gcc cct ggt ggc agg tcc ctc aac tgc ctg gtc aat ggc tcc ctc cac     1263
127 Ala Pro Gly Gly Arg Ser Leu Asn Cys Leu Val Asn Gly Ser Leu His
128         385                 390                 395
130 atc agc agc agc ctg gtg ccc atg cat cag ggg tcc ctg gcc gcc ggg     1311
131 Ile Ser Ser Ser Leu Val Pro Met His Gln Gly Ser Leu Ala Ala Gly
132     400                 405                 410
134 ccc tgt ggc tgc tgc tcc agc tgc ctg aac att ggg agc aaa gga aag     1359
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135 Pro Cys Gly Cys Cys Ser Ser Cys Leu Asn Ile Gly Ser Lys Gly Lys
136 415                 420                 425                 430
138 tcc tcc tac tgc tct gag ccc aca ctc ctc aaa aag gcc aac aaa aaa     1407
139 Ser Ser Tyr Cys Ser Glu Pro Thr Leu Leu Lys Lys Ala Asn Lys Lys
140                 435                 440                 445
142 cag aac ttc aag tcg gag gtc atg gta cca gtt aaa gcc agt ggc agc     1455
143 Gln Asn Phe Lys Ser Glu Val Met Val Pro Val Lys Ala Ser Gly Ser
144             450                 455                 460
146 tcc cac tgc cgg gca ggg cag act gga gtc tgt ctc att atg t           1498
147 Ser His Cys Arg Ala Gly Gln Thr Gly Val Cys Leu Ile Met
148         465                 470                 475
150 gattcctgga gcctgtgcct atgtcactgc aattttcagg agacatattc aactcctctg   1558
151 ctcttccaaa cctggtgtct atccggcaga gggaggaagg cagagcaagt ggagcagggc   1618
152 ttagcaggag cagtttctgg ccagaagcac cagcctgctg ccagcggggc agcccctcat   1678
153 aggaggccca ggagggagcc ccaaggcgta gaagccttgt tgaagctgtg agcaggagaa   1738
154 gcggtgccca ccagcttcca ggtctccctg acctgcctgc tctatgcccc acaccctacg   1798
155 tgccgtggct ctgtgcagtg tacgtagata gctctcgcct gggtctgtgc tgtttgtcgt   1858
156 gaaaagctta atgggctggc caggctgtgt caccttctcc aagcaaagcc atatggagca   1918
157 tctacccaga ctcccactct gcacacactc actcccacct ctcaagcctc caacctcttg   1978
158 gccagattgg gctcattaat gtcgttgcct gcccatctgc atgaatgaca ggcagctccc   2038
159 catggtggtc tgcctgtgag ctcttcaagt tctaatcctt aactccagga ttagctccca   2098
160 agtgcgctga gacccagcca gcacacttct ggcccttctc cctgcctcaa tctaaaagca   2158
161 gtgccacacc ctccaaagtg gaatagaaag aagttcatga gtaagggctg caaggaattc   2218
162 ttatcctggc cacatgtcct ccgtgcacac acccaatgga gttaaccttg gaagttgact   2278
163 attttaatgt ctgccaggag ttctaatcct gcctctgttc ccttttctct ccttgaaagt   2338
164 ccagcacacc attcttgtcc ttccccagtt tcctcgccct ccacccctcc agcttcatgc   2398
165 tcagtgttgt gcttaataaa atggacatat ttttctctaa aaaaaaaaa               2447
167 <210> SEQ ID NO: 2
168 <211> LENGTH: 476
169 <212> TYPE: PRT
170 <213> ORGANISM: H. sapiens
172 <400> SEQUENCE: 2
173 Met Gly Arg Lys Glu Glu Asp Asp Cys Ser Ser Trp Lys Lys Gln Thr
174  1               5                  10                  15
175 Thr Asn Ile Arg Lys Thr Phe Ile Phe Met Glu Val Leu Gly Ser Gly
176             20                  25                  30
177 Ala Phe Ser Glu Val Phe Leu Val Lys Gln Arg Leu Thr Gly Lys Leu
178         35                  40                  45
179 Phe Ala Leu Lys Cys Ile Lys Lys Ser Pro Ala Phe Arg Asp Ser Ser
180     50                  55                  60
181 Leu Glu Asn Glu Ile Ala Val Leu Lys Lys Ile Lys His Glu Asn Ile
182 65                  70                  75                  80
183 Val Thr Leu Glu Asp Ile Tyr Glu Ser Thr Thr His Tyr Tyr Leu Val
184                 85                  90                  95
185 Met Gln Leu Val Ser Gly Gly Glu Leu Phe Asp Arg Ile Leu Glu Arg
186             100                 105                 110
187 Gly Val Tyr Thr Glu Lys Asp Ala Ser Leu Val Ile Gln Gln Val Leu
188         115                 120                 125
189 Ser Ala Val Lys Tyr Leu His Glu Asn Gly Ile Val His Arg Asp Leu
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Output Set: N:\CRF3\10102001\I960643.raw

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190     130                 135                 140
191 Lys Pro Glu Asn Leu Leu Tyr Leu Thr Pro Glu Glu Asn Ser Lys Ile
192 145                 150                 155                 160
193 Met Ile Thr Asp Phe Gly Leu Ser Lys Met Glu Gln Asn Gly Ile Met
194                 165                 170                 175
195 Ser Thr Ala Cys Gly Thr Pro Gly Tyr Val Ala Pro Glu Val Leu Ala
196             180                 185                 190
197 Gln Lys Pro Tyr Ser Lys Ala Val Asp Cys Trp Ser Ile Gly Val Ile
198         195                 200                 205
199 Thr Tyr Ile Leu Leu Cys Gly Tyr Pro Pro Phe Tyr Glu Glu Thr Glu
200     210                 215                 220
201 Ser Lys Leu Phe Glu Lys Ile Lys Glu Gly Tyr Tyr Glu Phe Glu Ser
202 225                 230                 235                 240
203 Pro Phe Trp Asp Asp Ile Ser Glu Ser Ala Lys Asp Phe Ile Cys His
204                 245                 250                 255
205 Leu Leu Glu Lys Asp Pro Asn Glu Arg Tyr Thr Cys Glu Lys Ala Leu
206             260                 265                 270
207 Ser His Pro Trp Ile Asp Gly Asn Thr Ala Leu His Arg Asp Ile Tyr
208         275                 280                 285
209 Pro Ser Val Ser Leu Gln Ile Gln Lys Asn Phe Ala Lys Ser Lys Trp
210     290                 295                 300
211 Arg Gln Ala Phe Asn Ala Ala Ala Val Val His His Met Arg Lys Leu
212 305                 310                 315                 320
213 His Met Asn Leu His Ser Pro Gly Val Arg Pro Glu Val Glu Asn Arg
214                 325                 330                 335
215 Pro Pro Glu Thr Gln Ala Ser Glu Thr Ser Arg Pro Ser Ser Pro Glu
216             340                 345                 350
217 Ile Thr Ile Thr Glu Ala Pro Val Leu Asp His Ser Val Ala Leu Pro
218         355                 360                 365
219 Ala Leu Thr Gln Leu Pro Cys Gln His Gly Arg Arg Pro Thr Ala Pro
220     370                 375                 380
221 Gly Gly Arg Ser Leu Asn Cys Leu Val Asn Gly Ser Leu His Ile Ser
222 385                 390                 395                 400
223 Ser Ser Leu Val Pro Met His Gln Gly Ser Leu Ala Ala Gly Pro Cys
224                 405                 410                 415
225 Gly Cys Cys Ser Ser Cys Leu Asn Ile Gly Ser Lys Gly Lys Ser Ser
226             420                 425                 430
227 Tyr Cys Ser Glu Pro Thr Leu Leu Lys Lys Ala Asn Lys Lys Gln Asn
228         435                 440                 445
229 Phe Lys Ser Glu Val Met Val Pro Val Lys Ala Ser Gly Ser Ser His
230     450                 455                 460
231 Cys Arg Ala Gly Gln Thr Gly Val Cys Leu Ile Met
232 465                 470                 475
235 <210> SEQ ID NO: 3
236 <211> LENGTH: 25
237 <212> TYPE: DNA
238 <213> ORGANISM: H. sapiens
240 <400> SEQUENCE: 3
241 gtggagggcg aggaaactgg ggaag                                    25
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/960,643

DATE: 10/10/2001
TIME: 12:54:43

Input Set : A:\Seqlist.txt
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<210> SEQ ID NO: 4
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 4
ggagggcgag gaaactgggg aag 23

<210> SEQ ID NO: 5
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 5
gtggagggcg aggaaactgg ggaag 25

<210> SEQ ID NO: 6
<211> LENGTH: 31
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 6
ctcgagtcac ataatgagac agactccagt c 31

<210> SEQ ID NO: 7
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 7
Lys Arg Arg Glu Ile Leu Ser Arg Arg Pro Ser Tyr Arg
1 5 10

<210> SEQ ID NO: 8
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 8
Pro Leu Ala Arg Thr Leu Ser Val Ala Gly Leu Pro Gly Lys Lys
1 5 10 15

<210> SEQ ID NO: 9
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 9
Pro Leu Ser Arg Thr Leu Ser Val Ser Ser
1 5 10

<210> SEQ ID NO: 10
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 10
gaattcaatg ggtcgaaagg aagaagatga 30

<210> SEQ ID NO: 11
<211> LENGTH: 31
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

VERIFICATION SUMMARY DATE: 10/10/2001
PATENT APPLICATION: US/09/960,643 TIME: 12:54:44

Input Set : A:\Seqlist.txt
Output Set: N:\CRF3\10102001\I960643.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application Number
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date